

Genetic Analysis of Dairy Cattle Production Traits in a Management Intensive Rotational Grazing Environment

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ABSTRACT

Management intensive rotational grazing is a low input form of dairy herd management that is practiced by an increasing number of US dairy producers. However, concerns exist regarding the predictability of progeny performance in a grazing environment because most US dairy sires are progeny tested under conventional conditions of herd management. Lactation data from 27 Wisconsin dairy herds that have practiced management intensive rotational grazing for at least 4 yr were analyzed, as were data from three randomly chosen groups of control herds. Coefficients of regression of progeny milk, fat, and protein yields on USDA sire PTA values were 0.99, 0.76, and 0.96, respectively, from the grazing herds. In the control herds, regression coefficients for milk, fat, and protein yields averaged 0.95, 0.98, and 0.88, respectively. Therefore, progeny performance of grazing herds was predicted adequately by national sire PTA values that were derived primarily from conventionally managed herds. Heritability estimates for milk, fat, and protein yields were 0.23, 0.17, and 0.26, respectively, in the grazing herds and 0.24, 0.27, and 0.27, respectively, in a pooled data set containing all control herds. Estimated genetic correlations between production traits in the grazing environment and in the control environment were 0.92, 0.88, and 0.99 for milk, fat, and protein yields, respectively. These correlations, as well as the regression coefficients, indicate that interaction of genotype by environment is not important for these management systems, and nearly optimal genetic progress can be achieved by selecting AI sires progeny tested under traditional management conditions.

(**Key words:** grazing, genetics, genotype by environment interaction)

Abbreviation key: MIRG = management-intensive rotational grazing.

INTRODUCTION

Management intensive rotational grazing (**MIRG**) is gaining popularity in the US as a low input form of management of dairy herds. Costs of feed, capital equipment, and labor can be reduced substantially, which often leads to greater net profit, even if total milk production per cow decreases. Although the majority of US dairy farms use pasture to supplement the ration at specific times during the year, MIRG operations are typically defined as farms where the livestock harvest at least half of the forage annually. The MIRG farms are further characterized by frequent movement, or rotation, of the milking herd among pasture units or paddocks. Many MIRG operations practice seasonal calving to maximize pasture utilization although, in cold climates, a portion of the forage is often harvested mechanically and stored for winter use. In contrast, conventional US dairy operations are generally characterized by mechanical harvesting and storage of forages and a 12-mo milking schedule.

The interaction of genotype by environment (i.e., differential expression of animal genotype in a different climate or management system) can occur in two ways: 1) a scaling effect on phenotypic performance across environments or 2) a change in the genetic ranking of animals across environments. Scaling effects can generally be handled adequately by standardization of records (e.g., using a heterogeneous variance adjustment). However, changes in the ranking of selection candidates across environments results in a genetic correlation of <1 between environments. In such a situation, genetic evaluations of sires calculated in one environment may not be adequate predictors of progeny performance in another environment.

Although numerous studies have investigated interactions of genotype by environment involving different livestock breeds or different geographical regions, the present study focused on interactions of genotype by management system within a particular breed and climate.

Nearly 40 yr ago, Robertson et al. (5) recognized a conflict regarding the management conditions under which genetic selection decisions should be made. At

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that time, two opposing viewpoints existed for selection: 1) selection should be made at a high level of management to manifest genetic differences fully, and 2) selection should occur under commercial conditions to avoid incorrect decisions. Robertson et al. (5) reported genetic correlations ranging from 0.87 to 0.96 between British Friesian herds grouped into low, medium, or high management levels and concluded that there was no need to provide special strains within breeds that were specifically suited to herds of different production levels. Bondoc and Smith (1) later noted that this conflict was of particular importance with respect to nucleus breeding schemes.

Changes in genetic rankings of sires between conventional (confinement) and MIRG operations can be considered as a special case of the interaction between genotype and the level of concentrate (grain) that is provided in the ration. In an analysis of lactation records from the northeastern US, Wiggans and Van Vleck (8) concluded that the interaction between sire progeny group and the proportion of net energy provided by concentrates was unimportant. Waheed et al. (6) also found no evidence of an interaction between sire progeny group and the roughage source or the level of grain that was fed in Illinois Holstein herds.

In Ireland, Dillon and Crosse (3) reported no interaction between dairy cows of high (imported) genetic merit and cows of low (local) genetic merit that were fed either high or low amounts of supplemental concentrates in a rotational grazing system. In general, the high genetic merit cows were found (3) simply to have had greater intake of both forages and concentrates, a result supported by Grainger et al. (4) in a New Zealand grazing trial. Also, in Ireland, Cromie et al. (2) reported minimal interaction of genotype by environment between the top 25% and bottom 25% of dairy herds nationally using data based on concentrate input per cow per year. Estimated genetic correlations between performance of high input and low input herds were 0.92, 0.89, and 0.91 for yields of milk, fat, and protein, respectively.

In contrast, Wang et al. (7) reported a significant interaction between sire progeny group and level of concentrate feeding in Canadian Holstein cattle. However, those results may have been biased because cows in those experimental herds were fed concentrates individually according to their level of milk production.

Because most US AI sires are progeny tested under conventional management conditions, it is important to determine whether genetic superiority demonstrated in these confinement systems is expressed in

herds that practice MIRG. Therefore, the objective of the present study was to assess the magnitude of interactions of genotype by environment that may exist in Wisconsin dairy herds with differing management practices.

MATERIALS AND METHODS

Milk production data of Wisconsin dairy herds were provided by AgSource, Inc. (Verona, WI). Herds that practiced MIRG were identified using financial survey data collected by the University of Wisconsin Center for Dairy Profitability. Herds that reported that at least 50% of annual forage intake was harvested by the livestock for at least 4 yr consecutively were considered as being MIRG operations. Twenty-seven MIRG herds that had DHI milk recording information available from 1991 to the present were included in the study. In addition, three groups of control herds were selected at random from the AgSource database.

The phenotypic performance of progeny in MIRG and control herds was examined using linear regression of mature equivalent 305-d lactation yield of daughters on August 1997 USDA PTA values of their sires. Only AI-sired Holstein cows that calved from 1991 to 1995 were included in the regression analysis. Cows with unusually short (<75 d) or unusually long (>450 d) lactations were excluded. The following univariate linear regression model was fitted separately to data from the MIRG group and each of the three control groups:

$$y_{ijkl} = h_i + ys_j + p_k + \beta PTA_{ijkl} + e_{ijkl}$$

where

y_{ijkl} = mature equivalent milk, fat, or protein yield for a lactation of cow l in herd i , year-season of calving j , and parity k ,

h_i = fixed effect of herd i ,

ys_j = fixed effect of the year-season of calving j ,

p_k = fixed effect of the parity k ,

β = coefficient of regression of daughter lactation yield on sire PTA,

PTA_{ijkl} = August 1997 USDA milk, fat, or protein PTA of the cow's sire, and

e_{ijkl} = random residual term.

The genetic parameters for lactation performance of grazing and control herds were estimated by multiple-trait REML in an animal model with repeated records using VCE 3.2 software (9). The data were analyzed separately for milk, fat, and pro-

tein yields using a bivariate model that considered 305-d mature equivalent lactation yield in grazing herds and control herds as two separate traits. To reduce the number of genetic correlation parameters and, hence, the standard errors of the correlation estimates, data from all three control groups were pooled prior to variance component estimation. Thus, the REML analysis included 9987 lactation records (2606 from MIRG herds and 7381 from control herds) from 5339 Holstein cows. The model for variance component estimation was as follows:

$$y_i = x_i' \beta + z_{1i}' a + z_{2i}' p + e_i$$

where

- y_i = $n_i \times 2$ matrix of grazing and control lactation records for animal i (where n_i = number of records for animal i),
- x_i = $p \times n_i$ incidence matrix relating records of animal i to management group (herd-year-season) effects,
- β = $p \times 2$ matrix of fixed management group effects,
- z_{1i} = $q_1 \times n_i$ incidence matrix relating records of animal i to animal additive genetic effects,
- a = $q_1 \times 2$ matrix of random animal additive genetic effects for grazing and control performance,
- z_{2i} = $q_2 \times n_i$ incidence matrix relating records of animal i to permanent environmental effects,

- p = $q_2 \times 2$ matrix of random permanent environmental effects for grazing and control performance, and
- e_i = $n_i \times 2$ matrix of uncorrelated random residual effects corresponding to records of animal i .

The number of young sires that must be progeny tested in MIRG herds each year to exceed the level of genetic progress afforded by selecting among US AI sires was calculated as follows. The generation interval and genetic variance were assumed to be constant. The reliability of sire genetic evaluations in each environment was assumed to be 0.8, and the genetic correlation between the MIRG and control environments was assumed to be 0.7, 0.8, or 0.9. Therefore, accuracy was 0.894 (i.e., square root of reliability) for sires tested in MIRG herds and 0.626, 0.716, or 0.805 (i.e., square root of [reliability \times (genetic correlation)²]) for sires tested in control herds. It was assumed that 10, 25, or 50 elite sires were chosen each year from 1250 total sires tested in the control environment, so the fraction selected was 0.008, 0.02, or 0.04, respectively. The genetic progress that was achieved by using sires that were tested in the control environment was calculated as accuracy \times selection intensity. The selection intensity factor, fraction selected, and total number of sires that must be tested in the MIRG environment to achieve an equivalent rate of genetic progress were obtained by backsolving.

TABLE 1. Summary of data from grazing and control herds.

Variable	Group			
	Grazing	Control 1	Control 2	Control 3
Lactation records, no.	5621	6713	6238	5173
Cows, no.	2762	3163	3227	2534
Herds, no.	27	35	34	35
Mean mature equivalent milk, kg	8848	9100	9809	8659
Mean mature equivalent fat, kg	327	349	369	339
Mean fat percentage, %	3.69	3.83	3.76	3.91
Mean mature equivalent protein, kg	286	289	316	275
Mean protein percentage, %	3.24	3.18	3.22	3.18
Spring calvings (March–May), %	40	23	23	25
Mean calving interval, mo	13.0	13.5	14.1	13.8
Breed composition, %				
Holstein	93.9	96.7	95.7	92.8
Jersey	1.9	0.9	4.0	0.1
Brown Swiss	3.3	0.0	0.1	6.6
Guernsey	0.0	3.2	0.0	0.0
Ayrshire	0.2	0.0	0.0	0.1
Other	0.8	0.0	0.1	0.0

TABLE 2. Coefficients of regression of mature equivalent yield over a 305-d lactation on August 1997 USDA sire PTA values in the grazing and control herds.

Trait	Herd group							
	Grazing		Control 1		Control 2		Control 3	
		SE		SE		SE		SE
Milk	0.99	0.09	1.00	0.08	0.89	0.11	0.95	0.12
Fat	0.76*	0.10	0.96	0.09	1.01	0.11	0.96	0.12
Protein	0.96	0.09	0.85	0.09	0.94	0.11	0.86	0.12

*Different from 1.00 ($P < 0.05$).

RESULTS AND DISCUSSION

A summary of the data is shown in Table 1. Mean values for mature equivalent milk yield, protein yield, and protein percentage were similar for the MIRG and control herds. However, mature equivalent fat yield and fat percentage were lower for the MIRG herds. As expected, the mean calving interval was shorter in the MIRG herds because many MIRG herds practice seasonal calving. Differences in breed composition between MIRG and control herds were minimal.

Coefficients of regression of progeny performance on USDA sire PTA values are shown in Table 2. Regression coefficients for milk and protein yields were near 1 (their expectation) for both MIRG and control herds, which indicates that lactation milk and protein yields of the progeny of AI sires in MIRG herds were predicted adequately by USDA values for sire PTA, even though these PTA were calculated primarily from data of nongrazing herds. For fat yield, however, the regression coefficient for the MIRG herds was significantly lower than 1 (0.76). A possible explanation for the lower regression coefficient for fat and the lower mean fat yield and percentage in MIRG herds is that fat percentage may be adversely affected by variation in pasture quality throughout the grazing season.

Estimates of heritabilities and genetic correlations are shown in Table 3. Estimates of heritability of milk and protein yield were nearly identical in the MIRG and control herds. However, the heritability of fat yield was significantly lower (0.17) in the MIRG herds than in the control herds (0.27). Again, this result may be due to the effects of pasture quality on fat percentage. Because no cows had lactation records in both MIRG and control herds, estimated correlations were largely based on genetic relationships through sires that were used in both environments. There were 409 sires with progeny in both the MIRG and control (pooled) data sets; the mean number of progeny for these sires was 7.3 in the control data set and 3.8 in the MIRG data set. The estimated genetic

correlations between the MIRG herds and the control herds for milk, fat, and protein yields were 0.92, 0.88, and 0.99, respectively (approximate standard errors were 0.10), indicating that production in grazing and control (confinement) environments are highly correlated traits. This result is in agreement with the results of Cromie et al. (2).

The MIRG herds in the present study were required to participate in DHI milk recording programs. Therefore, this particular group of MIRG herds might have a different management level than Wisconsin MIRG herds as a whole, and this group may contain a higher proportion of transitional grazing operations (i.e., confinement dairies that have switched to rotational grazing). However, the same criteria regarding DHI participation were applied to the control herds, so conclusions regarding the predictability of progeny performance in MIRG and conventional dairy operations and estimates of genotype by management system interaction should be valid.

It has been suggested (Carl Fredericks, 1998, personal communication) that graziers should cooperate in the development of a dairy sire sampling scheme so that young sires could be tested for progeny performance under MIRG conditions. However, because of the high correlation between grazing and confinement

TABLE 3. Estimates of heritability (on diagonal) and genetic correlations (above diagonal) for mature equivalent milk, fat, and protein yields over a 305-d lactation in the grazing and control herds (control groups 1, 2, and 3 were pooled) using multiple-trait REML.

Trait	Herd group			
	Grazing		Control	
		SE		SE
Milk	0.23	0.04	0.92	0.10
			0.24	0.03
Fat	0.17	0.04	0.88	0.10
			0.27	0.03
Protein	0.26	0.04	0.99	0.10
			0.27	0.03

TABLE 4. Number of young sires that must be sampled each year under management intensive rotational grazing conditions to achieve the same level of genetic progress offered by selecting among the 1250 AI sires currently sampled each year in the US.

Genetic correlation ¹	Evaluated sires needed		
	10	25	50
0.90	570	670	750
0.80	280	370	460
0.70	140	220	300

¹Between grazing and confinement environments.

performance, an extremely large sampling program would be needed for MIRG-based sires to exceed the rate of genetic progress that can be achieved by using US AI sires. Table 4 shows the number of young sires that must be sampled annually in MIRG herds to reach the same level of genetic progress afforded by selecting among the 1250 AI sires currently sampled each year in the US. If genetic correlations between grazing and confinement environments are approximately 0.9, as reported by Cromie et al. (2) and the present study, graziers must sample 600 to 700 young bulls annually. A sampling scheme of this magnitude would be prohibitively expensive and would likely be impossible, given the current number of grazing operations in the US. With genetic correlations near and greater than 0.9, a high rate of genetic progress can be achieved in the grazing environment by selecting sires that have been evaluated under conventional management conditions.

Although many US graziers choose to select dairy sires that were progeny tested in another country with perceived similarities in herd management (e.g., New Zealand or Ireland), this method of selection may not lead to greater genetic progress for two reasons. First, differences between countries in climate or in genetic background of the cow population may actually reduce (rather than increase) the predictability of progeny performance. In fact, the estimated genetic correlation for milk yield between the US and New Zealand of 0.76 (INTERBULL Centre, Uppsala, Sweden, 1998, personal communication) is much lower than the genetic correlation between MIRG and confinement operations reported in the present study. Second, the number of young sires sampled annually in countries such as New Zealand or Ireland is substantially fewer than the number sampled in the US; therefore, a significant reduction in selection intensity would occur.

CONCLUSIONS

Rotational grazing is currently practiced by a small but increasing number of US dairy farmers, and con-

cerns exist about the predictability of progeny performance of AI sires when these sires are tested under conventional management conditions. Analysis of lactation data from Wisconsin herds that utilize MIRG indicates that progeny performance in a grazing system can be adequately predicted by PTA of sires calculated from data of herds that do not follow this practice. In addition, results of the present and previous (2) studies indicate that the genetic correlation for milk production traits between grazing and confinement environments is extremely high. For these reasons, development of a special scheme for progeny testing bulls under MIRG conditions does not appear to be warranted. Graziers will maximize genetic progress by selecting among the top AI sires internationally rather than by restricting selection to sires from countries where MIRG is commonly practiced. However, development of national genetic evaluations for male and female reproductive traits would be of benefit to graziers who practice seasonal calving to maximize pasture utility.

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